REMARKS

Applicants have amended the claims to make explicit that what was implicit. For example, the claims have been amended to recite "an ordered array of immobilized oligonucleotides in the array's x and y corrdinates with multiple copies of a sequence of interest extending in the array's z dimension" rather than a "redundant array" to more explicitly define that the oligonucleotides are extended in the z dimension. Claims 11 and 23 and 30 have been amended to clearly indicate that each oligonucleotide is described by an x, y, and z coordinate, with a 5' end attached to a solid support (i.e. at a x,y position) and extends in the z dimension. Claims 11, 23 and 30 have also been amended to clearly state that the 3' end of the original, unextended oligonucleotide is copied each time the sequence of interest is copied. These amendments are supported by pages 10 -11 of the specification and do not introduce new matter; their entry is respectfully requested.

Claims 11 and 23-38 stand rejected under 35 U.S.C. §102(e) as being anticipated by Smith et al., U.S. Patent No. 5,753,439, filed May 19, 1998 ("Smith").

Applicants respectfully disagree and submit that the rejection should be withdrawn for the following reasons.

The Examiner argues that the claimed ordered arrays are taught by Smith, which allegedly describes an array comprising 10-10,000 probes with 2-2000 repeats in each probe.

Applicants disagree because the Smith array requires 5'- and 3'-ends that are complementary to the target nucleic acid being screened and an intervening sequence that is not. One consequence of this structural requirement for the Smith probes is that it renders the arrays of the present invention completely different, because the applicants' arrays would not function in Smith's assays because they do not meet this requirement. In taking this position, the Examiner totally ignores that structured requirement of the array of Smith. This is a substantial difference between the array of Smith and the present arrays. Thus, the array of Smith teaches that its probes have a top and bottom

portion, each of which is complementary to the target nucleic acid that contains a sequence of interest and a middle portion that is not. If the Smith array had an intervening portion that could bind the 5' or 3' end of the sequence of interest then the Smith array could not be used for its intended purpose. In contrast, the array formed herein does not have such a requirement.

More specifically, the present invention provides arrays which have oligonucleotides bound to a solid support at a position defined by its x and y coordinates, where each oligonucleotide has <u>multiple copies of a sequence of interest</u>. The multiple copies are referred to in the claims and the specification as redundant in the z dimension, or as "multiple copies of a sequence of interest extending in the z dimension" (e.g., claims 11 and 23). To create this array, one begins with an array of oligonucleotides bound to a solid surface at their 5' ends. These initial unextended oligonucleotides only contain <u>one copy</u> of the sequence of interest, and sometimes only a <u>portion of one copy</u> of the sequence of interest. Moreover, the 3' end of the original oligonucleotide (or probe) of the present invention is complementary to a portion of the sequence of interest on the circular DNA template. Thus, when this initial oligonucleotide is extended, its 3'end which is complementary to the circular DNA target is copied each time the target is copied. Thus, for final arrays of claim 11 and 23, each oligonucleotide must have at least two copies of the sequence at its 3' end. In other words, in the applicants' arrays, the oligonucleotides' **<u>3' ends are</u> <u>never unique sequences</u>** within that oligonucleotide's sequence: the 3' sequence is always found within the same oligonucleotide at a position along its z axis which is closer to the solid support. Claim 30 similarly states that the 3' end is not unique from the intervening repeats.

In contrast, while the Smith arrays can contain repeated sequences, as indicated by the Examiner, the repetition can NEVER extend all the way to the 3' end of the probe or the array will not function for its intended use. The function of the Smith array requires that its 3' end is complementary to the 5' end of its target nucleic acid (and requires similar complementarity at its opposite end). If the sequence of the Smith 3' end was also present at an internal region of the probe, that is if the 3' end was repeated, then the oligonucleotide could bind its target in multiple configurations, which would generate

a multitude of different signals following strand displacement, and thus interfere with the function of the array. Thus, the function of the Smith array imposes a structural requirement on its oligonucleotide probes, which is that the oligonucleotides' **3' ends are always unique sequences** within that oligonucleotide's sequence.

This difference between the Smith array and the applicants' array is illustrated in the attached Figure (Appendix 1). This Figure illustrates that while both arrays can contain repeated units along the z axis for their oligonucleotides, there is a fundamental and critical difference in these repeated units. The applicants's array with have repetition of its 3' end internally, while the Smith array can **never** have repetition of its 3' ends.

In light of the above, Applicants respectfully submit that Smith does not include all the elements of the Applicants' claims and that the rejection of the claims under 35 U.S.C. § 102(b) over Smith should therefore be withdrawn.

For the reasons discussed and stated above, and herein incorporated by reference, Applicants respectfully submit that the Examiner's argument regarding claim 30, claims 24-29, and 31-33, are similarly addressed. Therefore, applicants submit that the rejections of claims 30, 24-29, and 31-33 should be withdrawn.

Accordingly, in view of the foregoing, Applicants respectfully submit that all claims comply with 35 U.S.C. § 102(e).

In view of the foregoing, applicants submit that all claims are in condition for allowance. Early and favorable action is requested.

Respectfully submitted,

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